Getting started with coding and R

Stirling Coding Club

30 October 2024

Stirling Coding Club

"Coding Club is for everyone, regardless of their career stage or current level of knowledge. Coding Club is a place that brings people together, regardless of their gender or background. We all have the right to learn, and we believe learning is more fun and efficient when we help each other along the way." – Edinburgh Coding Club

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- ▶ Participate as much or as little as you prefer!

Stirling Coding Club in 2023-2024

1. 30 OCT 2024: Getting started in R
2. 13 NOV 2024: General computing concepts (and more R)
3. 27 NOV 2024: Writing and using functions in R
4. 22 JAN 2025: Writing and using loops in R
5. 05 FEB 2025: Simulating data in R
6. 19 FEB 2025: Writing slides in Rmarkdown
7. 05 MAR 2025: Writing manuscripts in Rmarkdown
8. 19 MAR 2025: Introduction to Rshiny apps
9. 02 APR 2025: Randomisation approaches in R
10. 16 APR 2025: Writing tests for code
11. 30 APR 2025: Individual-based modelling in R
12. 14 MAY 2025: Introduction to version control

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https://stirlingcodingclub.github.io/studyGroup/

Do I need to learn how to code?

Is this a necessary skill in the sciences?

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[1]Dreyfuss (2017). Wired.
https://www.wired.com/2017/03/biologists-teaching-code-survive/.
[2]Mike (2019). https://mikethemadbiologist.com/2019/12/06/biologists-should-not-learn-how-to-code/.

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Not only is coding a core skill that gets the basic work of biology done, it's also taught [biologists] to look at problems in new ways. Above all, they agree, **coding liberated them**. As tools evolve to allow biologists to gather ever-more-massive quantities of data, people [...] will find a way to make coding a core part of scientific education[1].

[T]here's nothing wrong with becoming an expert (or close to one) in a given skill set (e.g., statistics, coding), and **it also will be a good thing as a biologist**. But I don't think coding will be the must-have skill set a few years from now (except for those who develop new tools)[2].

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How does coding (specifically R) help me as a researcher?

Most scientific research relies on numeric data.

- ▶ Data organisation
- ▶ Statistical analysis
- ▶ Visualisation

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Software exists that can do the above without code.

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Practical advantages of using these software tools

- ▶ Graphical User Interface (no need to work with code).

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- ▶ **Write your own statistical analyses**
- ▶ **Create your own plots**

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A lot of coding is Googling solutions to get the code to work.

Write your own solutions to data organisation problems

```
##            SPEI Year Tree_ID      BAI cumul_mn
## 1  0.34325052 1966  FR6201 645.3972       NA
## 2 -1.35933830 1967  FR6201 470.0363       NA
## 3  0.49415034 1968  FR6201 830.5755       NA
## 4 -1.38069918 1969  FR6201 414.0594       NA
## 5  0.79613295 1970  FR6201 977.4877       NA
## 6 -0.06371012 1971  FR6201 809.8834       NA
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Calc. the cumul_mn for the BAI col. every year for each tree[1]:

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[1]Thanks to Tom Ovenden for letting me use this example.

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Calc. the cumul_mn for the BAI col. every year for each tree[1]:

▶ Do not include *current* BAI record in cumul_mn calc
▶ If the Year SPEI is >1 or -1, never include the BAI value
▶ If the Year − 1 SPEI is >1 or <-1, never include the BAI value
▶ If the Year − 2 SPEI is >1.5 or <-1.5, never include the BAI value
▶ If the Year − 3 SPEI is >2 or <-2, never include the BAI value

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Write your own solutions to data organisation problems

Solution took 65 lines of code written in 3 custom functions.

```
tree_cumulative_mean <- function(dat){
    trees      <- unique(dat$Tree_ID);
    new_table <- NULL;
    for(tree in trees){
        sub_dat    <- dat[dat$Tree_ID == tree,];
        tree_cumul <- get_cumulative(tree = sub_dat);
        new_tree   <- update_cumul(tree = sub_dat,
                                    vec  = tree_cumul);
        new_table  <- rbind(new_table, new_tree);
    }
    return(new_table);
}
```

The above is the 'outermost' function.

Write your own statistical analyses

Testing the effects of fig tree spatial distributions on pollinator, seed, and parasite distributions.

[1] Duthie AB, Nason JD (2016) *Oikos* 125(11):1597-1606.

Write your own statistical analyses

```
##   Year Site Tree Poll Npoll Seeds       Vol      Lat
## 1 2010  170    6    0    22    NA  753.6000 28.24057
## 2 2010  170    6    0    10    NA 1025.7333 28.24057
## 3 2010  170    6    7    37    NA 1047.7133 28.24057
## 4 2010  170    6    0    36    NA 1230.8800 28.24057
## 5 2010  170    6    0    34    NA  884.4333 28.24057
## 6 2010  170    6    0    33    NA 1128.3067 28.24057
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- ▶ Needed to use mean tree values and a custom index of fig wasp dispersal ability
- ▶ Wanted to make analysis open source and figures reproducible
- ▶ Had to help a colleague use the same analysis on new data

Create your own plots
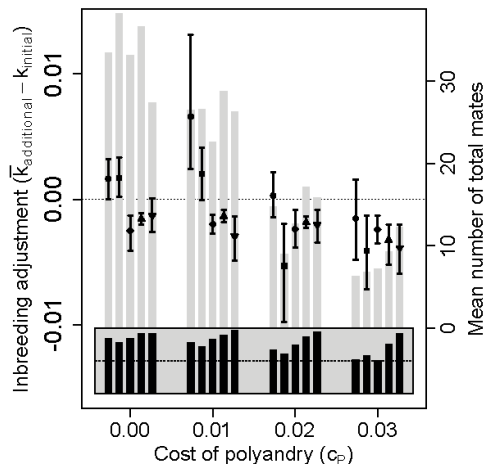
Custom built plot with R code for an individual-based model.

[1]Duthie AB, et al. (2016) *Evolution* 70(9), 1927–1943.

R is extremely useful for doing scientific research

A bit of coding skill can save a lot of time in the long run.

- ▶ You do not need to know everything
- ▶ Help is available from many places

https://stirlingcodingclub.github.io/getting_started/notes.html

https://ourcodingclub.github.io/tutorials/intro-to-r/

https://ourcodingclub.github.io/tutorials/troubleshooting/